

FIGURE 1

CTGTCTGCCCATCTGAATAACAAGAGATGGGGCTTGTGATTTTCCTCCACGGTTCTGGGT  
 1 -----+-----+-----+-----+-----+-----+-----+ 60  
 GACAGACGGGTAGACTTATTTGTCTCTACCCCGAACACTAAAAGGAGGTGCCAAGACCCA

C M G L V I F L H G S G S -

CTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCTGAAGGGCTCCAGGCTC  
 61 -----+-----+-----+-----+-----+-----+-----+ 120  
 GACCATTACTTCAGTATCTTCCGGGGTCTTACGTTGTGAGGACTTCCCAGGGTCCGAG

C G N E V I E G P Q N A T V L K G S Q A R -

GCTTCAACTGCACCGTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGG  
 121 -----+-----+-----+-----+-----+-----+-----+ 180  
 CGAAGTTGACGTGGCAGAGGGTCCCGACCTTCAGTAGTACACCCGAGAGTCACTGTACC

C F N C T V S Q G W K L I M W A L S D M V -

TGGTGCTAAGCGTCAGGCCCCATGGAGCCCATCATCACAATGACCGCTTACCTCTCAGA  
 181 -----+-----+-----+-----+-----+-----+-----+ 240  
 ACCACGATTGCAAGTCCGGGTACCTCGGGTAGTAGTGGTTACTGGCGAAGTGGAGAGTCT

C V L S V R P M E P I I T N D R F T S Q R -

GGTACGACCGAGGGCGGGAATTCACCTCGGAGATGATCATCCACAAATGTGGAGCCCATG  
 241 -----+-----+-----+-----+-----+-----+-----+ 300  
 CCATGCTGTGTCGCCCTTGAAGTGGAGCTCTACTAGTAGTGTTACACCTCGGCTCAC

C Y D Q G G N F T S E M I I H N V E P S D -

ATTCGGGGAACATCAGATGTCAGCCTCCAGAACAGTGCCTGCATGGATCTGCTTACCTTA  
 301 -----+-----+-----+-----+-----+-----+-----+ 360  
 TAAGCCCCCTGTAGTCTACGTGAGGCTTGTGACGGACGTACCTAGACGAATGGAAT

C S G N I R C S L Q N S R L H G S A Y L T -

CCGTCCAAGTTATGGGAGAGCTGTTTCATTCACAGTGTTAATCTTGTAGTCGTGAGATG  
 361 -----+-----+-----+-----+-----+-----+-----+ 420  
 GGCAGGTTCAATACCTCTCGACAAGTAAGGGTCACAATTAGAACATCAGCGACTCTTAC

C V Q V M G E L F I P S V N L V V A E N E -

AACCTTGTGAAGTTACTTGTCTACCTCACACTGGACCCGGCTCCCGGATATTTCTGGG  
 421 -----+-----+-----+-----+-----+-----+-----+ 480  
 TTGGAACTTCAATGAACAGATGGGAGTGTGACCTGGGCCGAGGGCTATAAAGGACCC

C P C E V T C L P S H W T R L P D I S W E -

AGCTCGGTCTCCTGGTCAGCATTCAAGCTATTATTTGTTCCGGAGCCAGCGACCTTC  
 481 -----+-----+-----+-----+-----+-----+-----+ 540  
 TCGAGCCAGAGGACAGTGGTAAGTTCGATAATAAAACAAGGCCCTCGGGTCTGCTGGAAG

C L G L L V S H S S Y Y F V P E P S D L Q -

AAAGTCAGTGAGCATCTGGCTCTGACCCACAGAGCAATGGGACTTTGACTTGCGTGG  
 541 -----+-----+-----+-----+-----+-----+-----+ 600  
 TTTCAGTCACTCGTAGGACCGAGACTGGGGTGTCTGTTACCTGAAACTGAACGGACC

C S A V S I L A L T P Q S N G T L T C V A -



FIGURE 2

1 AGTGATCATGGTGGCAGGAGCCATGAAAAATAGAGACCCACCGGTTCTGGGTCTGGTAA  
 TCACTAGTACCACCGTCTCGGTACCTTTATCTCTGGGTGGGCAAGACCCAGACCATT 60  
 b M V A G A M E N R D P P G S G S G N -  
 61 TGAAGTCATAGAAGGCCCCAAAATGCAAGAGTCTGAAGGGCTCCAGGCTCGCTTCAA  
 ACTTCAGTATCTCCGGGGTTTTACGTCTCAGGACTTCCGAGGGTCCGAGCGAAGTT 120  
 b E V I E G P Q N A R V L K G S Q A R F N -  
 121 CTGCACCGTCTCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGTCT  
 GACGTGGCAGAGGGTCCCGACCTTCGAGTAGTACACCCGAGAGTCACTGTACCACCACGA 180  
 b C T V S Q G W K L I M W A L S D M V V L -  
 181 AAGCGTCAGGCCCATGGAGCCCATCATCACCATGACCGCTTCACCTCTCAGAGGTACGA  
 TTCGCAGTCCGGGTACCTCGGGTAGTAGTGGTTACTGGCGAAGTGGAGAGTCTCCATGCT 240  
 b S V R P M E P I I T N D R F T S Q R Y D -  
 241 CCAGGGCGGGAATTCACCTCGGAGATGATCATCCACAATGTGGAGCCCACTGATTCGGG  
 GGTCCCGCCCTTGAAGTGGAGCCTCTACTAGTAGGTGTACACCTCGGGTCACTAAGCCC 300  
 b Q G G N F T S E M I I H N V E P S D S G -  
 301 GAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTACCCTCCA  
 CTTGTAGTCTACGTCGGAGGTCTTGTACGCGGACGTACCTAGACGAATGGAATGGCAGGT 360  
 b N I R C S L Q N S R L H G S A Y L T V Q -  
 361 AGTTATGGGAGAGCTGTTTCACTCCAGTGTTAATCTTGTAGTTCGCTGAGAATGAACCTTG  
 TCAATACCTCTCGACAAGTAAGGGTCACAATTAGAACATCAGCGACTCTTACTTGAAC 420  
 b V M G E L F I P S V N L V V A E N E P C -  
 421 TGAAGTTACTTGTCTACCTCAGCTGGACCTGGCTCCCGGATATTTCTCTGGGAGCTCGG  
 ACTTCAATGAACAGATGGGAGTGTGACCTGGACCGAGGGCTATAAAGGACCTCGAGCC 480  
 b E V T C L P S H W T W L P D I S W E L G -  
 481 TCTCTGGTACGCCATTCAGCTATTATTTGTTCCGGAGCCACGACCTTCAAAGTGC  
 AGAGGACCAGTCGGTAAGTTCGATAATAAAACAAGGCCTCGGGTCTGCTGGAAGTTTCAGG 540  
 b L L V S H S S Y Y F V P E P S D L Q S A -  
 541 AGTGAGCATCTGGCTCTGACCCACAGAGCAATGGGACTTTGACTTTCGCTGGCTACCTG  
 TCACTCTGAGGACCGAGACTGGGGTGTCTCGTTACCTTGAACTGAACGCACCGATGGAC 600  
 b V S I L A L T P Q S N G T L T C V A T W -

FIGURE 2 (con't)

601 G A A G A G C C T G A A G G C C C G A A G T C T G C A A C T G T A A A T C T C A C T G T G A T T C C G G T G T C C C C A  
C T T C T C G G A C T T C C G G G C G T T C A G A C G T T G A C A T T T A G A G T G A C A C T A A G C C A C A G G G G T 660

b K S L K A R K S A T V N L T V I R C P Q -

661 A G A C A C T G G A G T G G T A T T A A T A T T C C A G G T G A T T A T C A A G T T T A C C G A G T T T A G G T T T  
T C T G T G A C C T C C A C C A T A A T T A T A G G T C C A C A T A A T A G T T C A A A T G G C T C A A A T C C A A A 720

b D T G G G I N I P G V L S S L P S L G F -

721 T T C A T T G C C T A C T T G G G G C A A A G T T G G A C T T G G A C T A G C A G G C A C C A T G C T T C T G A C G C C  
A A G T A A C G G A T G A A C C C C G T T T C A A C C T G A A C C T G A T C G T C C G T G T A C G A A G A C T G C G G 780

b S L P T W G K V G L G L A G T M L L T P -

781 G A C G T G T A C T C T T A C A A T A C G T G C T G C T G C C G C C G T C G T T G T G T G G C T G C A A C T G  
C T G C A C A T G A G A A T G T T A T G C G A C G A C G A C G C G G C G C A G A C A A C A C C G A C G T T G A C 840

b T C T L T I R C C C C R R R R C C G C N C -

841 C T G C T G C C G T T G T T T T C T G C T G T A G A G A A A A G A G G A T T C G T A T T C A A T T T C A A A A  
G A C G A C G G C A A C A A A G A C G A C A T C T T C T T T T C T C C T A A A G C A T A A G T T A A A G T T T T 900

b C C R C C F C C R R K R G F R I Q F Q K -

901 G A A A T C T G A A A A G A G A A G A C A A A A A G A A A C T G A G A C A G A A A G T G G A A A T G A A A A C T C  
C T T T A G A C T T T T T C T C T C T G T T G T T T C T T T G A C T C T G T C T T T C A C C T T T A C T T T T T G A G 960

b K S E K E K T N K E T E T E S G N E N S -

961 C G G C T C A A T T C A G A T G A C A A A A G A C C A G A C A C C G T T C T C T C C C T C C C A A A T C C T G  
G C C G A T G T T A G T C T A C T T G T T T C T G T G T C T G T G G C G A A G A G A G G G A G G G T T T A G G A C 1020

b G Y N S D E Q K T T D T A S L P P K S C -

1021 T G A A T C C A G T G A T C C T G A C A A A A A C A G T A G C T G T G G C C C T C C T C A C C A G C G G G C T G A  
A C T T A G G T C A C T A G G A C T T G T T T C T T T G T C A T C G A C A C C G G A G A G T G G T C G C C C G A C T 1080

b E S D P E Q R N S S C G P P H Q R A D -

1081 T C A A C G T C C A C C A G C C A G C A A G T C A T C C A C A G G C T T C T T T A A T C T G G C C A G T C C T G A  
A G T T G C A G G T G G G T C C G G T C G T T C A G T A G G T T C C G A A G A A A A T T A G A C C G G T C A G G A C T 1140

b Q R P P R P A S H P Q A S F N L A S P E -

1141 G A A G S T C A G T A A T A C A A C T G T A G T A T A G 1168  
C T T C C A G T C A T T A T G T T G A C A T C A T A T C

b K V S N T T V V \* -

●

[illegible]

FIGURE 3 (con't)

1201 GGCCAGTCCTGAGAAGGTCAGTAATACAACCTGTAGTATAG  
-----+-----+-----+-----+ 1240  
CCGGTCAGGACTCTTCCAGTCATTATGTTGACATCATATC

b                    A   S   P   E   K   V   S   N   T   T   V   V   \*

[illegible]

FIGURE 4

1 ATGGTGGCAGGAGCCATGGAAAAATAGAGACCCACCCGGTTCTGGGTCTGGTAATGAAGTC  
 TACCACCGTCTCTGGTACCTTTATCTCTGGGTGGGCCAAGACCCAGACCATTAATCTCAG 60  
 a M V A G A M E N R D P P G S G S G N E V -  
 61 ATAGAAGGCCCCCAAAATGCAAGAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACC  
 TATCTTCCGGGGGTTTACGTTCTCAGGACTTCCCGAGGGTCCGAGCGAAGTTGACGTGG 120  
 a I E G P Q N A R V L K G S Q A R F N C T -  
 121 GTCTCCAGGGCTGGAAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTCTAAGCGTC  
 CAGAGGGTCCCGACCTTCGAGTAGTACACCCGAGAGTCACTGTACCACCAGCATTCGCAG 180  
 a V S Q G W K L I M W A L S D M V V L S V -  
 181 AGGCCCATGGAGCCCATCATCACCATGACCGCTTCACCTCTCAGAGGTACGACCAAGGC  
 TCCGGGTACCTCGGTAGTAGTGGTTACTGGCGAAGTGAAGAGTCTCATGCTGGTCCCG 240  
 a R P M E P I I T N D R F T S Q R Y D Q G -  
 241 GGGAACTCACCTCGGAGATGATCATCCACAATGTGGAGCCAGTGATTCGGGGAACATC  
 CCCTTGGAGTGGAGCCTCTACTAGTAGGTGTACACCTCGGTCACCTAAGCCCTTGTAG 300  
 a G N L T S E M I I H N V E P S D S G N I -  
 301 AGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGTTATG  
 TCTACGTCCGAGGTCTTGTGACGGACGTACCTAGACGAATGGAATGGCAGGTTCATAAC 360  
 a R C S L Q N S R L H G S A Y L T V Q V M -  
 361 GGAGAGCTGTTTATCCAGTGTTAATCTTGTAGTCGTCGAGAATGAACCTTGTGAAGTT  
 CCTCTCGACAAGTAAGGGTCAAAITAGAACATCAGCGACTCTTACTTGGAACTTCAA 420  
 a G E L F I P S V N L V V A E N E P C E V -  
 421 ACTTGCTACCTCACACTGGACCCGGCTCCCGGATATTCTCGGGAGCTCGGTCTCCTG  
 TGAACAGATGGGAGTGTGACCTGGGCCGAGGGCTATAAAGGACCTCGAGGCAGAGGAC 480  
 a T C L P S H W T R L P D I S W E L G L L -  
 481 GTCAGCCATCAAGCTATTATTTGTTCGGGAGCCGACGACCTTCAAAGTGCAGTGAGC  
 CAGTCGGTAAAGTTTCGATAATAAAACAAGGCCTCGGGTCGCTGGAAGTTTCAGTCACTCG 540  
 a V S H S Y Y F V P E P S D L Q S A V S -  
 541 ATCCTGGCTCTGACCCACAGAGCAATGGGACTTTGACTTGCCTGGCTACCTGGAAGAGC  
 TAGGACCGAGACTGGGGTGTCTCGTTACCTGAAACTGAACGACCGATGGACCTTCTCG 600  
 a I L A L T P Q S N G T L T C V A T W K S -

FIGURE 4 (con't)

601 CTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATTCGGTGTCCCCAAGACACT  
 GACTTCCGGGCGTTTCAGACGTTGACATTTAGAGTGACACTAAGCCACAGGGTTCTGTGA 660  
 a L K A R K S A T V N L T V I R C P Q D T -  
 661 GGAGGTGGTATTAAATATTCAGGTGTATTATCAAGTTTACCGAGTTTAGGTTTTTCATTG  
 CCTCCACCATAATTATAAGGTCCACATAAATAGTTTCAAATGGCTCAAATCCAAAAGTAAC 720  
 a G G G I N I P G V L S S L P S L G F S L -  
 721 CCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGTGT  
 GGATGAACCCCGTTTCAACCTGAACCTGATCGTCCGTGGTACGAAGACTGCGGCTGCACA 780  
 a P T W G K V G L G L A G T M L L T P T C -  
 781 ACTCTTACAATACGCTGTCTGTCTGCCGCCGTCTTTGTTGTGGTGTCAACTGCTGCTGC  
 TGAGAATGTTATGCGACGACGACGACGGCGGCAGCAACAACACCGACGTTGACGACGAGC 840  
 a T L T I R C C C C R R R C C G C N C C C -  
 841 CGTGTGTGTTTCTGTGTAGAGAAGAAAAGAGGAAATCTGAAAAAGAGAAGACAAACAAAG  
 GCAACAACAAGACGACATCTCTTTTCTCTTTAGACTTTTCTCTTCTGTTTGTGTTT 900  
 a R C C F C C R R K R G N L K K R R Q T K -  
 901 AAAGTGTGAGACAGAAAGTGAAATGAAAATCCGGCTACAATTCAGATGAACAAAAGACCA  
 TTTGACTCTGTCTTTCACCTTTACTTTTGAGGCCGATGTTAAGTCTACTTGTGTTTCTGGT 960  
 a K L R Q K V E M K T P A T I Q M N K R P -  
 961 CAGACACCGCTTCTCTCCCTCCCAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACA  
 GTCTGTGGCGAAGAGAGGGAGGTTTAGGACACTTAGGTCACTAGGACTTGTGTTCTTTGT 1020  
 a Q T P L L S L P N P V N P V I L N K E T -  
 1021 GTAGCTGTGGCCCTCCTCACCAGCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATC  
 CATCGACACCGGAGGAGGTGTCGCCGACTAGTTGACGGTGGGTCCGGTCTGTTAGTAG 1080  
 a V A V A L L T S G L I N V H P G Q Q V I -  
 1081 CACAGGCTTCTTTTAATCTGGCCAGTCTCGAAGGTCAGTAATACAACGTAGTATATA  
 GTGTCCGAAGAAAATAGACCGGTGAGGACTCTTCCAGTCATTATGTTGACATCATATT 1139  
 a H R L L L I W P V L R R S V I Q L \*



FIGURE 5

1 GTGAACGAGATACAGAGATTTACCTGCCTGAGGTAAGGAAGATCATGCTGAGATGGAGGG  
 CACTTGCTCTATGTCTCTAAATGGACGGACTCCATTCTCTAGTACGACTCTACCTCCC 60

b M E G -

61 CAGCTGGAGAGATGTCTGGCTGTGCTGGTCATCTGGCTCAGCTGACAGCTTCCGGATC  
 GTCGACCTCTCTACAGGACCGACACGACCACTAGGACCGAGTCGACTGTCTGAAGGCTTAG 120

b S W R D V L A V L V I L A Q L T A S G S -

121 CAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCTTAAAGGACTCAGAGGCTCA  
 GTCAATAGTCTAGTATCTTCCAGGAGTCTTACATTGTCTCAGGATTCTCTGAGTCTCCGAGT 180

b S Y Q I I E G P Q N V T V L K D S E A H -

181 CTTCAACTGCACCTGACTCACGGCTGGAAGCTTCTCATGTGGACTCTTAACCAATGGT  
 GAAGTTGACGTGGCACTGAGTGCCGACCTTCGAAGAGTACACCTGAGAATTGGTTTACCA 240

b F N C T V T H G W K L L M W T L N Q M V -

241 GGTGCTGAGTCTCACCAACCAAGGACCCATCATCACCAACAACCGCTTACCTATGCCAG  
 CCACGACTCAGAGTGGTGGGTTCTGGGTAGTAGTGGTTGTCGCAAGTGGATACGGTC 300

b V L S L T T Q G P I I T N N R F T Y A S -

301 TTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATGTGACGCCCAGTGA  
 AATGTTGTCGTGACTGTGCAAGTAGAGCTCAACTAGTAGGTACTACACGTCGGGTCACT 360

b Y N S T D S F I S E L I I H D V Q P S D -

361 CTCGGGATCCGTGCAATGCAGCCTCAGACAAGCCATGGGTTTGGATCTGCCTTCCTCTC  
 GAGCCCTAGGCACGTTACGTCCGACGTCTTGTCGGTACCCAAACCTAGACGGAAGGAGAG 420

b S G S V Q C S L Q N S H G F G S A F L S -

421 AGTCAAAGTCATGGGGACCCCTGAACATTCTAGCAACAACCTTATAGTCACTGAGGGTGA  
 TCACGTTCACTACCCCTGGGACTTGTAAGGATCGTGTGTGGAATATCAGTGACTCCCACT 480

b V Q V M G T L N I P S N N L I V T E G E -

481 ACCCTGTAATGTGACTTGCTATGCCGTGGGCTGGACCTCACTCCCGGATATTCTCTGGGA  
 TGGGACATTACACTGAACGATACGGCACCCGACCTGGAGTGAGGGCTATAAAGGACCTT 540

b P C N V T C Y A V G W T S L P D I S W E -

541 GCTTGAGGTTCCCGTAAGCCATTGAGTTACAATTCTTTCTGGAGCCGGGCAACTTTAT  
 CGAAGCTCCAAGGGCATTCGGTAAGCTCAATGTTAAGGAAAGACCTCGGCCCGTTGAAATA 600

b L E V P V S H S S Y N S F L E P G N F M -

FIGURE 5 (cont)

601 GAGGGTCTTGAGTGTCTCTGGACCTCACACCACTGGGCAACGGGACCTTGACTTGTGTGGC 660  
 CTCCAGAACTCACAGGACCTGGAGTGTGGTGACCCGTTGCCCTGGAACCTGAACACACCC  
 b R V L S V L D L T P L G N G T L T C V A -  
 661 AGAGCTGAAGGACTTGCAGGCCAGCAAGTCCTTAACCTGCAACCTGACTGTGGTTACGCC 720  
 TCTCGACTTCTCTGAACGTCGGGTGTTTCAGGAATTGACAGTTGGACTGACACCAAGTCCG  
 b E L K D L Q A S K S L T V N L T V V Q P -  
 721 TCCACCTGACAGTATTGGAGAGGAAGGCCAGCACTGCCGACCTGGGCCATCATCTCTGCT 780  
 AGGTGGACTGTCTAATCTCTCTCTCCGGGTGTCGACGGCTGGACCCGGTAGTAGGACGA  
 b P P D S I G E E G P A L P T W A I I L L -  
 781 GGCAGTGGCCTTTTCTCTTGTCTTGTATCTGATCATTTGTTTATTATAATATTCTGTGTG 840  
 CCCTCACCGGAAAAGGAACGAGAAGTGGACTAGTAACAAAATAATATTATAAGACAAAC  
 b A V A F S L L L I L I I V L I I I F C C -  
 841 CTGTTGTGCCTCCAGGAGAGAAAAGGAAGAACTTACTTATCAAAATGAAATAAGGAAATC 900  
 GACAACACGGAGGTCTCTCTTTCTCTTCTAGATGAATAGTTTACTTTATTCTCTTTAG  
 b C C A S R R E K E E S T Y Q N E I R K S -  
 901 TGCAAAACATGAGGACAAAACAGAGATCCGGAGACAAAGTTAAAAAGTGAAAGGAAAA 960  
 ACGTTTGTACTCTCTGTTTGTCTCTAGGCCTCTGTTTCAATTTTTCACCTTTCTCTTT  
 b A N M R T N K A D P E T K L K S G K E N -  
 961 CTACGGGTACAGTTCGGATGAGGCAAGGCTGCACAGACTGCATCTCTCCCTCCTAAATC 1020  
 GATGCCCATGTCAAGCCTACTCCGTTTCCGACGTGTCTGACGTAGAGAGGAGGATTAG  
 b Y G Y S S D E A K A A Q T A S L P P K S -  
 1021 TGCTGAAGTCAGCCTTCCAGAAAAACGAGCAGTAGCCTTCTCTTATCAGGAACCTCAATAA 1080  
 ACGACTTCAGTCGGAAGGTCTTTTTCGCGTCGTATCGGAAGGAATAGTCTTGAGTTATT  
 b A E V S L P E K R S S S L P Y Q E L N K -  
 1081 ACATCAGCCCGGTCAGCAACTCATCCAGGGTTTTCCTTTGACATCGCCAGTCTCTCAGAA 1140  
 TGTAGTCGGGCCAGGTCTGAGTAGGTGCCCAAAGGAACTGTAGCGGTGAGGAGTCTT  
 b H Q P G P A T H P R V S F D I A S P Q K -  
 1141 GGTGCAAAATGTGACTTTAGTGTAAATAAGACTTCTCATGACTGTACTTGGTGCA 1195  
 CCAGTCTTTACACTGAAATCACATTATTTCTGAAGAGTACTGCATGAACACGT  
 b V R N V T L V \*

FIGURE 6

1 GTGAACGAGATACAGAGATTTACCTGCCTGAGGTAAGGAAGATCATGCTGAGATGGAGGG  
 CACTTGCTCTATGTCCTAAATGGACGGACTCCATTCTCTAGTACGACTCTACCTCCC 60  
 b M E G -  
 61 CAGCTGGAGAGATGTCTCTGGCTGTGCTGGCTCATCTGGCTCAGCTGACAGCTTCCGGATC  
 GTCGACCTCTCTACAGGACCGACACGACCAGTAGGACCGAGTCGACTGTCTGAAGCCCTAG 120  
 b S W R D V L A V L V I L A Q L T A S G S -  
 121 CAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCTCTAAAGGACTCAGAGGCTCA  
 GTCAATAGTCTAGTATCTTCCAGGAGCTTACATTGTCAGGATTCCTGAGTCTCCGAGT 180  
 b S Y Q I I E G P Q N V T V L K D S E A H -  
 181 CTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTCTTAACCAAAATGGT  
 GAAGTTGAGCTGGCAGTCTGAGTGCCGACCTTCGAAGAGTACACCTGAGAATTTGGTTACCA 240  
 b F N C T V T H G W K L L M W T L N Q M V -  
 241 GGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCACCAACCGCTTACCTATGCCAG  
 CCACGACTCAGAGTGGTGGGTCTCTGGGTAGTAGTGGTTGTTGGCGAAGTGAGTACGCTC 300  
 b V L S L T T Q G P I I T N N R F T Y A S -  
 301 TTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATGTGCAGCCCCAGTGA  
 AATGTTGCTGACTGTGCAAGTAGAGCCTCACTAGTAGTACTACAGCTGGGTCCT 360  
 b Y N S T D S F I S E L I I H D V Q P S D -  
 361 CTCGGGATCCGTGCAATGCAGCCTGCAGAACGCCATGGGTTGGATCTGCCTTCTCTC  
 GAGCCCTAGGCACGTTACGTCGGACGCTTGTCTGGTACCCAAACCTAGACGGAAGGAGAG 420  
 b S G S V Q C S L Q N S H G F G S A F L S -  
 421 AGTGCAAGACAGTATTGGAGAGGAAGGCCAGCACTGCCGACCTGGGCCATCATCTGCT  
 TCACGTTCTGTGATCAACCTCTCTTCCGGGTCTGACGGCTGGACCCGGTAGTAGGACGA 480  
 b V Q D S I G E E G P A L P T W A I I L L -  
 481 GGCAGTGGCCTTTTCTTGTCTTGTATCTGATCATTTGTTTGTATTATAATATTCTGTTG  
 CCGTACCCGAAAGGAACGAGACTAGGACTAGTAACAAAACCTAATATTATAAGACAAC 540  
 b A V A F S L L I L I I V L I I I F C C -  
 541 CTGTTGTGCCCTCAGGAGAGAAAAGGAAGAATCTACTTATCAAAATGAAATAAGGAAATC  
 GACAACACGGAGTCTCTCTTTTCTTCTTAGATGAATAGTTTACTTTATTCTCTTAG 600  
 b C C A S R R E K E E S T Y Q N E I R K S -  
 601 TGCAAAATGAGGACAAACAAAGCAGATCCGAGACAAAGTTAAAAGTGGAAGGAAAA  
 ACGTTTGTACTCTCTTTGTTCTGCTTAGGCCTCTGTTTCAATTTTACCTTTCTTTT 660  
 b A N M R T N K A D P E T K L K S G K E N -



CTACGGGTACAGTTCGGATGAGGCCAAGGCTGCACAGACTGCATCTCTCCCTCCTAAATC  
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----720  
GATGCCCATGTCAAGCCTACTCCGTTTCCGACGTGTCTGACGTAGAGAGGGAGGATTTAG

721 TGCTGAAGTCAGCCTTCCAGAAAAACGCAGCAGTAGCCTTCCTTATCAGGAACCTCAATAA  
-----+-----+-----+-----+-----+-----+-----+  
ACGACTTCAGTCGGAAGGTCTTTTGCCTCGTCATCGGAAGGAATAGTCCTTGAGTTATT 780

781 ACATCAGCCCGGTCCAGCAACTCATCCACGGGTTTCCTTTGACATCGCCAGTCCCTCAGAA  
-----+-----+-----+-----+-----+-----+-----+-----  
TGTAAGTCGGGCCAGGTCTGTTGAGTAGGTGCCCAAAGGAAACTGTAGCGGTACAGGATCTTT 840

841 GGT CAG AAT GTG ACT TTA CTG TAA TAA GAC TTA CTG ACT GTG TACT TGG TGC A  
-----+-----+-----+-----+-----+-----+-----+----- 895  
CCAGTCTTTACACTGAAATCACATTATTTCTGAAGAGTACTGACATGAACACCGT

[illegible]

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[illegible]

FIGURE 7 (con't)

601 AAAACGCAGCAGTAGCCTTCCCTTATCAGGAACCAATAAACATCAGCCCGTCCAGCAAC  
-----+-----+-----+-----+ 660  
TTTTCGCTCCTCATCGGAAGGAATAGTCCCTGAGTTATTTGTAGTCGGGCCAGGTCGTTG

b K R S S S L P Y Q E L N K H Q P G P A T -

661 TCATCCACGGGTTTCCTTTGACATCGCCAGTCCAGAAAGTCAGAAATGTGACTTTAGT  
-----+-----+-----+-----+ 720  
AGTAGGTGCCCAAAGGAACTGTAGCGGTCAGGAGTCTTCCAGTCTTTTACACTGAAATCA

b H P R V S F D I A S P Q K V R N V T L V -

721 GTAATAAAGACTTCTCATGACTGTACTTGGTGCA  
-----+-----+-----+ 754  
CATTATTTCTGAAGAGTACTGACATGAACCACGT

b \*

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FIGURE 8

1 .....MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQ 32  
 1 MAYSCQPLQESPLLGFPLRFIHLFVL.LLVGLLQI.SSGIVGQVSKSVR 48  
 33 NVTVLKDEAHFNCTVTHGWKLLMWTNLNQMVVLSLTTOGPPII...TNNRF 79  
 49 EKALL.SCDYKF.CSEEQSIHRIYWQKHDKMVLVSIISGVPEVWPKYKNRT 96  
 80 TYASYNSTDSFISELIIHDVQPSDSGSGVQCSLQNSHGFGSAFL....SVQ 125  
 97 VYDIANNYSFSLGLIL.....SDRGTYTCVVQRYEG.GSYVVKHLTTVE 140  
 126 VMGTNLNIPSNLIIVTEGEP.C....NVTYAVGWTSPLDISWELEVPSHS 171  
 141 LSVRADFPTPN.ITEYGNPSADIKRITCFASGGFPKPRLSW.LENGRELN 188  
 172 SYNSFL..EP.GNFMRVLSVLDLTPLGNGTLTCVAELKDLQASKSLTVNL 218  
 189 GINTTISQDPESELYTIISSQLDFNATYDHFIDCFIEYGDHVSQ....NF 234  
 219 TVVQPPPDSSIGEEGPALPTW.....AIIILLAVAFSLLLILIIIVLIIF 261  
 235 TWVKPPEDPPDEKQTVPFAGPDAVKAIIIFFIAITVIAIAIAIIIF 284  
 262 CCCASRR.EKEESTYQNEIRKSANMRTNKADPETKLKSGKENYGYSSDE 310  
 285 CITVKFRRCFRRRNEASRETNKNLYIGPVEAAAEQTV..... 321



FIGURE 9

1 .....MGLVIFLHSGSGNEVIEGPQNATVLKGSQARFNCTVSQ 39  
 1 MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQNVTVLKDSEAHFNCTVTH 50  
 40 GWKLIMWALS DMVVL SVRPM EPIITNDRFTS QRYDQGGNFT SEMIHNVE 89  
 51 GWKLLMWTLNQMVVLSLT TQGP IITNNRFTYASYNSTD SFISELIIHDVQ 100  
 90 PSDSGNIRCSLQNSRLHGSAYLT VQVMGELFIPSVNLVVAENEPCEVTCL 139  
 101 PSDSGSVQCSLQNSHGFGSAFLSVQVMGTLNIPSNLIVTEGEP CNVTCY 150  
 140 PSHWTRL PDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGLT 189  
 151 AVGWTSLEPDISWELEV PVSHSSYNSFLEPGNFM RVLSVLDLTP LGNGTLT 200  
 190 CVATWKS LKARKSATVNLTVIRCPQDTGGGINIPGVLSLPSLGFSLPTW 239  
 201 CVAELKDLQASKSLTVNLTVVQPPD.....SIGEEGPALPTW 238  
 240 GKVLGLAGTMLLTPTCTLTIRCCCCRRRCCGCCNCCRCFCRRKRGRFR 289  
 239 AIILLAVAFSLLLILIIIVLIIIFCCC.....CASR.....REKEEST 275  
 290 IQFQ.KKSEKEKTNK...ETETESGNENSGYNSDEOKTTDTASLPPKSC 335  
 276 YQNEIRKSANMRTNKADPETKLKSGKENYGYSSDEAKAAQTASLPPKSAE 325  
 336 SSDPEQRNSSCGPPHORADQRP RPASHPQASFNLASPEKVSNTTVV\* 383  
 326 VSLPEKRSSSL..PYQELNKHQPGPATHPRV SFDIASPQKVRNVTLV\* 371